

APPENDIX TO RESPONSE AND AMENDMENT

IN THE SPECIFICATION

N12B14
v - b 2nd Amendments to 1st full paragraph of Page 6:

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IDC-A1,AMD

"Extensive genetic analysis of resistant viral isolates generated through *in vivo* or *in vitro* selection has revealed that resistance is generally caused by mutations altering the nucleotide sequence at some specific site(s) of the viral genome. The mutational patterns that have been observed and reported for HIV-1 and that are correlated with drug resistance are very diverse: some antiretroviral agents require only one single genetic change, while others require multiple mutations for resistance to appear. A summary of mutations in the HIV genome correlated with drug resistance has been compiled. See Schinazi, R.F., Larder, B.A. & Meliors, J.W. 1997. Int. Antiviral News. 5, 129-142 (1997). Additionally, an electronic listing with mutations has also become available on the internet at sites such as hiv-web.lanl.gov or www.viralresistance.com [at http://hiv-web.lanl.gov or http://www.viralresistance.com]. Of course, as antiretroviral drugs are administered for longer periods of time, mostly in combination with each other, and as new antiretrovirals are being developed and added to the present drugs, new resistance-correlated genetic variants are being discovered. Of particular import is that the combination of antiretroviral agents can influence resistance characteristics."

IN THE CLAIMS

1 . (Amended) A method for determining the level of resistance of HIV to an HIV RT inhibitor comprising: